

Flag-peptide GAD65 Not I IA2 Sgf I PPINS poly-his
DYKDDDDK-----KKKRPRKKK-----KKRSRKKK-----CNGSHHHHHH

FIG. 1a

Flag-peptide GAD65 Not I IA2 Sgf I PPINS poly-his
DYKDDDDK-----KKKRPRKKK-----KKRSRKKK-----CNGSHHHHHH

FIG. 1b

MRRPRRPGGLGSGGLRLLLCLLSSRPGGCSAVSAHGCILFDRRLCSHLEVCIQDGLFGQCQVGVGQARPLLQVTPVLORL
QGVLRQLMSQGQLSWHDDLTQYVISQEMERIPRLPPEPRDRSGLAPKRPGPAGELLLQDIPITGSAPAQQHRLPQPPVGKGG
AGASSLSPLQAELLPPPLEHLLLPQPPPHPSLSYEPAALLQPFQDSGLLYLAQELPAPSRAARVPRLPEEQGSSSRRAEDSPGEGYEKEGLGDRGEKPASPAVQPDAA
FGDHPGHSYGDLPGPSPAQLFQDSGLLYLAQELPAPSRAARVPRLPEEQGSSSRRAEDSPGEGYEKEGLGDRGEKPASPAVQPDAA
QRLLAAVLAGYGVELRQLTPEQLSTLLQQLLPKGAGRNPQGVNVGADIKKTMEGPVEGRDTAELPARTSPMPGHPTASPT
SSEVQQPSPVSSSEPPKAARPPVTPVLEKKSPLGQSQPTVAGQPSARPAEEYGYIVTDQKPLSLAAGVKLLEILAEHVHMS
GSFINISVVGPAALTFRIRHNEQNLSSLADVTQQAGLVKSELLEAQATGLQILQTTGQVQOREAAAALPQTAHSTSPPMRSVLLTLVALA
GVAGLLVALVALCVRQHARQDQDKERLAALGPEGAHGDTTFEYQDLCRQHMATKSLFNRAEGPPPEPSRVSSVSSQFSDAAQ
ASPSHSSSTPSWCEEPAQANMDISTGHMILAYMEDHLRNNDRLAKEWQALCAQAEPNNTCATAQGEGENIKKNRHPDFLPHYDH
ARIKLKVESSPSRSRDYINASPIEHDPRMPAYIA TOGQPLSHTIADFQWMVWE SGCTVIVMLTPLVEDGVKOCDRYWPDEGASLY
HYYEVNLVSEHIWCDFLVRSEFYLKNUVTOETRTLTOFHFLSWPAEGTPASTRPLLDFRRKVNKCYRGRCSCPIVHCSDGAGR
IGTYLIDMVLNRMMAKGVKEDIAATLEHVDRDORPGLYRSKDFOFEALTAVAEVNAILKALPQ

FIG. 2a

MASPGSGFWSFGESEDGSGDSENPGTARAWCQVAQKFTGGIGNKLCALLYGDAEKPAESGGSQPPRAAARKAACACDQKPCS
CSKVVDVNYAFLHATTDLPAACDGERPTLAFLODVMNILLQOYVVKSFDRSTKVIDFHYPNELLOEYNWELADOPONLEEILMHC
OTLTKYAIKTGHPRYFNOLSTGIDMVGLAADWLTSTANTNMFTYEJAPVFLVLEYTLLKKMREIIGWPGSGDGIFSPGGAIS
NMYAMMIARFKMPEVKEKGMAALPRLIAFTSEHSHFSLKKGAALGIGTDSVLIKCDERGKMPSDLERRILEAKOKGFVPF
LVSATAGTIVYGAEDPLLAYADICKKYKIWMHVDAAWGGGLIMSRKHKWKLSGVERANSVTWNPHKMMGVPLOCSALLY
REEGLMONCNOMHASYLFOODKHYDLSYDTGDKALQCGGRHYDVKLWLMWRAKGTTGFEAHYDVKCLELAEYLYNHKNR
EGYEMVFDGKPOHINTVCFWYIPPSLRTLEDNBERMSRSLSKVAPPKARMMEYGTMTMVSYQPLGDKVNFFRMVISNPAATHQ
DIDFJEEUERLGDL

FIG. 2b

MALWMRLLPLALLALWGPDPAAAFVNQHILCGSHLVEALYLVCGERGFFYT
PKTRREAEDLQVQGQVELGGPGAGSLQPLALEGSLQKRGIVEQCCTSICSLYQ
LENYCN

FIG. 2c

1 ACCCGCCCTC GCCGCTCGGC CCCGCGCGTC CCCGCGCGTG CCCTCCCTCCC
51 GCCACACGGC ACGCACGCGC GCGCAGGGCC AAGCCGAGGC AGCCGCCCGC
101 AGCTCGCACT CGCTGGCGAC CTGCTCCAGT CTCCAAAGCC GATGGCATCT
151 CCGGGCTCTG GCTTTGGTC TTTGGGTG GAAGATGGCT CTGGGGATTG
201 CGAGAATCCC GGCACAGCGC GAGCCTGGTG CCAAGTGGCT CAGAAGTTCA
251 CGGGCGGCAT CGGAAACAAA CTGTGCGCCC TGCTCTACGG AGACGCCGAG
301 AAGCCGGCGG AGAGCGGCGG GAGCCAACCC CCGCGGGCCG CCGCCCGGAA
351 GGCGCCTGC GCCTGCGACC AGAACGCGT CAGCTGCTCC AAAGTGGATG
401 TCAACTACGC GTTCTCCAT GCAACAGACC TGCTGCCGGC GTGTGATGGA

451 GAAAGGCCA CTTTGGCGTT TCTGCAAGAT GTTATGAACA TTTTACTTCA
501 GTATGTGGTG AAAAGTTCG ATAGATCAAC CAAAGTGATT GATTCCATT
551 ATCCTAATGA GCTTCTCAA GAATATAATT GGGAAATTGGC AGACCAACCA
601 CAAAATTGG AGGAAATTG GATGCATTGC CAAACAACCTC TAAAATATGC
651 AATTAAAACA GGGCATCCTA GATACTCAA TCAACTTCT ACTGGTTGG
701 ATATGGTTGG ATTAGCAGCA GACTGGCTGA CATCAACAGC AAATACTAAC
751 ATGTTCACCT ATGAAATTGC TCCAGTATTG GTGCTTTGG AATATGTCAC
801 ACTAAAGAAA ATGAGAGAAA TCATTGGCTG GCCAGGGGGC TCTGGCGATG
851 GGATATTTC TCCCGGTGGC GCCATATCTA ACATGTATGC CATGATGATC
901 GCACCGTTA AGATGTTCCC AGAAGTCAAG GAGAAAGGAA TGGCTGCTCT
951 TCCCAGGCTC ATTGCCTCA CGTCTGAACA TAGTCATTG TCTCTCAAGA
1001 AGGGAGCTGC AGCCTAGGG ATTGGAACAG ACAGCGTGAT TCTGATTAAA
1051 TGTGATGAGA GAGGGAAAAT GATTCCATCT GATCTTGAAA GAAGGATTCT
1101 TGAAGCCAAA CAGAAAGGGT TTGTTCTT CCTCGTGAGT GCCACAGCTG
1151 GAACCACCGT GTACGGAGCA TTTGACCCCC TCTTAGCTGT CGCTGACATT
1201 TGCAAAAAGT ATAAGATCTG GATGCATGTG GATGCAGCTT GGGGTGGGG
1251 ATTACTGATG TCCCAGAAAC ACAAGTGGAA ACTGAGTGGC GTGGAGAGGG

FIG. 3a

1 CAGCCCTCT GGCAGGCTCC CGCCAGCGTC GCTGCGGCTC CGGCCCGGGA
51 GCGAGCGCCC GGAGCTCGA AAGATGCGGC GCCCGCGGCG GCCTGGGGT
101 CTCGGGGAT CGGGGGTCT CCGGCTGCTC CTCTGCCTCC TGCTGCTGAG
151 CAGCCGCCCG GGGGGCTGCA GCGCCGTAG TGCCCACGGC TGTCTATTG
201 ACCGCAGGCT CTGCTCTCAC CTGGAAGTCT GTATTAGGA TGGCTTGTT
251 GGGCAGTGCC AGGTGGGAGT GGGGCAGGCC CGGCCCTT TGCAAGTCAC
301 CTCCCCAGTT CTCCAACGCT TACAAGGTGT GCTCCGACAA CTCATGTCCC
351 AAGGATTGTC CTGGCACGAT GACCTCACCC AGTATGTGAT CTCTCAGGAG
401 ATGGAGCGCA TCCCCAGGCT TCGCCCCCA GAGCCCCGTC CAAGGGACAG
451 GTCTGGCTTG GCACCCAAGA GACCTGGTCC TGCTGGAGAG CTGCTTTAC
501 AGGACATCCC CACTGGCTCC GCCCCTGCTG CCCAGCATCG GCTTCCACAA
551 CCACCAGTGG GCAAAGGTGG AGCTGGGGCC AGCTCCTCTC TGTCCCTCT
601 GCAGGCTGAG CTGCTCCGC CTCTCTGGA GCACCTGCTG CTGCCCCAC
651 AGCCTCCCCA CCCTTCACTG AGTTACGAAC CTGCCTGCT GCAGCCCTAC
701 CTGTTCCACC AGTTGGCTC CCGTGATGGC TCCAGGGTCT CAGAGGGCTC
751 CCCAGGGATG GTCAGTGTG GCCCCCTGCC CAAGGCTGAA GCCCCTGCC
801 TCTTCAGCAG AACTGCCTCC AAGGGCATAT TTGGGGACCA CCCTGGCCAC
851 TCCTACGGGG ACCTTCAGG GCCTTCACCT GCCCAGCTT TTCAAGACTC
901 TGGGCTGCTC TATCTGGCCC AGGAGTTGCC AGCACCCAGC AGGGCCAGGG
951 TGCCAAGGCT GCCAGAGCAA GGGAGCAGCA GCCGGGCAGA GGACTCCCCA
1001 GAGGGCTATG AGAAGGAAGG ACTAGGGGAT CGTGGAGAGA AGCCTGCTTC
1051 CCCAGCTGTG CAGCCAGATG CGGCTCTGCA GAGGCTGGCC GCTGTGCTGG
1101 CGGGCTATGG GGTAGAGCTG CGTCAGCTGA CCCCTGAGCA GCTCTCCACA
1151 CTCCCTGACCC TGCTGCAGCT ACTGCCAAG GGTGCAGGAA GAAATCCGGG
1201 AGGGGTTGTA AATGTTGGAG CTGATATCAA GAAAACAATG GAGGGGCCGG
1251 TGGAGGGCAG AGACACAGCA GAGCTTCCAG CCCGCACATC CCCCATGCCT

FIG. 3c

1 CTCGAGGGGC CTAGACATTG CCCTCCAGAG AGAGCACCCA ACACCCCTCCA
51 GGCTTGACCG GCCAGGGTGT CCCCTTCCTA CCTTGGAGAG AGCAGCCCCA
101 GGGCATCCTG CAGGGGGTGC TGGGACACCA GCTGGCCTTC AAGGTCTCTG
151 CCTCCCTCCA GCCACCCCCAC TACACGCTGC TGGGATCCTG GATTCAGCT
201 CCCTGGCCGA CAACACTGGC AAACCTCTAC TCATCCACGA AGGCCCTCCT
251 GGGCATGGTG GTCCCTCCCA GCCTGGCAGT CTGTTCCCTCA CACACCTTGT
301 TAGTGCCCAG CCCCTGAGGT TGCAGCTGGG GGTGTCTCTG AAGGGCTGTG
351 AGCCCCCAGG AAGCCCTGGG GAAGTGCCTG CCTTGCCTCC CCCCCGGCCCT
401 GCCAGGCCCT GGCTCTGCCCT TCCTACCTGG GCTCCCCCA TCCAGCCTCC
451 CTCCCTACAC ACTCCTCTCA AGGAGGCACC CATGTCCTCT CCAGCTGCCG
501 GGCCTCAGAG CACTGTGGCG TCCTGGGCA GCCACCGCAT GTCCCTGCTGT
551 GGCATGGCTC AGGGTGGAAA GGGCGGAAGG GAGGGTCCT GCAGATAAGCT
601 GGTGCCCACT ACCAAACCCG CTCGGGGCAG GAGAGCCAAA GGCTGGGTGT
651 GTGCAGAGCG GCCCCGAGAG GTTCCGAGGC TGAGGCCAGG GTGGGACATA
701 GGGATGCGAG GGGCCGGGGC ACAGGATACT CCAACCTGCC TGCCCCCATG
751 GTCTCATCCT CCTGCTCTG GGACCTCCTG ATCCTGCCCT TGTTGCTAAG
801 AGGCAGGTAA GGGGCTGCAG GCAGCAGGGC TCGGAGCCCA TGCCCCCTCA
851 CCATGGGTCA GGCTGGACCT CCAGGTGCCT GTTCTGGGA GCTGGGAGGG
901 CCGGAGGGGT GTACCCCAGG GGCTCAGCCC AGATGACACT ATGGGGGTGA
951 TGGTGTCAATG GGACCTGGCC AGGAGAGGGG AGATGGGCTC CCAGAAGAGG
1001 AGTGGGGGCT GAGAGGGTGC CTGGGGGGCC AGGACGGAGC TGGGCCAGTG
1051 CACAGCTTCC CACACCTGCC CACCCCCAGA GTCCCTGCCGC CACCCCCAGA
1101 TCACACGGAA GATGAGGTCC GAGTGGCCTG CTGAGGACTT GCTGCTTGT
1151 CCCAGGTCCC CAGGTCATGC CCTCCTCTG CCACCCCTGGG GAGCTGAGGG
1201 CCTCAGCTGG GGCTGCTGTC CTAAGGCAGG GTGGGAACTA GGCAAGCCAGC
1251 AGGGAGGGGA CCCCTCCCTC ACTCCCACTC TCCCACCCCC ACCACCTTGG
1301 CCCATCCATG GCGGCATCTT GGGCCATCCG GGACTGGGGGA CAGGGGTCC
1351 GGGGACAGGG GTCCGGGGAC AGGGTCCTGG GGACAGGGGT GTGGGGACAG

FIG. 3f